

SEQUENCE LISTING

<110> Unilever plc

Unilever NV

<120> Production of Antibodies

<130> T7060

<160> 67

<170> PatentIn version 3.0

<210> 1

<211> 440

<212> DNA

<213> Artificial

<220>

<223> VHH with peptide linker

<220>

<221> CDS

<222> (1)..(417)

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Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly		
1				5					10				15			

tct	ctg	aga	ctc	tcc	tgt	gca	gcc	tcg	gga	cgc	gcc	acc	agt	ggt	cat		96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Ala	Thr	Ser	Gly	His		
20					25					30							

ggt	cac	tat	ggt	atg	ggc	tgg	ttc	cgc	cag	gtt	cca	ggg	aag	gag	cgt		144
Gly	His	Tyr	Gly	Met	Gly	Trp	Phe	Arg	Gln	Val	Pro	Gly	Lys	Glu	Arg		
35					40							45					

gag	ttt	gtc	gca	gct	att	agg	tgg	agt	ggt	aaa	gag	aca	tgg	tat	aaa		192
Glu	Phe	Val	Ala	Ala	Ile	Arg	Trp	Ser	Gly	Lys	Glu	Thr	Trp	Tyr	Lys		
50				55						60							

gac	tcc	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gat	aac	gcc	aag	act		240
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Thr		
65					70					75			80				

acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg gcc gtt	288
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val	
85 90 95	
 tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc ctg ccg	336
Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro	
100 105 110	
 gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc tcc tca	384
Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser	
115 120 125	
 gaa caa aaa ctc atc tca gaa gag gat ctg aat taataagggc taagctcgaa	437
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn	
130 135	
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 Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg	
35 40 45	
 Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys	
50 55 60	
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr	
65 70 75 80	
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val	
85 90 95	
 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro	
100 105 110	
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115 120 125	
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn	
130 135	

<210> 3

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<213> Artificial

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<400> 3

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
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<210> 4

<211> 471

<212> DNA

53303

<223> VHH with linker

<220>

<221> CDS

<222> (1) .. (459)

<400> 4

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Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1           5           10          15

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48

tct ctg aga ctc tcc tgt gta gct tct gaa agc agc ttc agc aac aat
 Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
 20 25 30

96

```

cac atg ggc tgg tac cgc cgg gct cca ggg aac cag cgc gag ctg gtc
His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
35          40          45

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144

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gca act att agt cct ggt ggt agc aca cac tat gta gac tcc gtg aag
Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
      50           55           60

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192

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ggc cga ttc acc atc tcc cga gac aac gcc aag aac aca gtg tat cta
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65           70           75           80

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240

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caa atg gac agc ctg aaa cca gag gac acg gcc gtc tat tac tgt gct
Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85          90          95

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288

100

105

110

ctg gtc acc gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg 384
 Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
 115 120 125

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gcc gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc      432
Ala Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
   130          135          140

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Ser Glu Glu Asp Leu Asn Gly Ala Ala
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<400> 5

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20 25 30

His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
 35 40 45

Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
115 120 125

Ala Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
130 135 140

Ser Glu Glu Asp Leu Asn Gly Ala Ala
145 150

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<220>
<221> CDS
<222> (1)..(456)

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Gln Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln Ala Gly Gly		
1 5 10 15		
tct ctg aga ctc tcc tgt gta gcc tct gga aac acc ttc agt atc ata		96
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile		
20 25 30		
gct atg gcc tgg tac cgc cag gct cca ggg aag cag cgc gag gtg gtc		144
Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val		
35 40 45		
gca agt att aat agt att ggc agc aca aat tat gca gac tcc gtg aag		192
Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys		
50 55 60		
ggg cga ttc acc atc tcc aga gac aac gcc aag aac aca gtg tat ctg		240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu		
65 70 75 80		
caa atg agc agc ctg aaa cct gag gac acg gcc gtc tat tac tgt gct		288
Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
85 90 95		
gcc ggt aat ttg ctg gtt aag agg cct tac tgg ggc cag ggg acc ctg		336
Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu		
100 105 110		
gtc acc gtc tcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc		384
Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala		
115 120 125		
gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca		432
Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser		
130 135 140		
gaa gag gat ctg aat ggg gcc gca tagtaacaat tg		468
Glu Glu Asp Leu Asn Gly Ala Ala		
145 150		

<210> 7

<211> 152

<212> PRT

<213> Artificial

<400> 7

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
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20 25 30

Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
35 40 45

Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
115 120 125

Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
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Glu Glu Asp Leu Asn Gly Ala Ala
145 150

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<220>

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1	5	10	15	
15				
gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc			96	
Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe				
20	25	30		
30				
agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt			144	
Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg				
35	40	45		
45				
gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg			192	
Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Arg Thr Tyr Tyr Ala				
50	55	60		
60				
gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac			240	
Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn				
65	70	75	80	
80				
acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt			288	
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val				
85	90	95		
95				
tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc			336	
Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr				
100	105	110		
110				
gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat			384	
Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His				
115	120	125		
125				
cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag			432	
His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu				
130	135	140		
140				
gat ctg aat ggg gcc gca tagtaacaat tg			462	
Asp Leu Asn Gly Ala Ala				
145	150			

<210> 9

<211> 150

<212> PRT

<213> Artificial

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20 25 30

Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
 35 40 45

Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
 50 55 60

Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
 65 70 75 80

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110

Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
 115 120 125

His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 130 135 140

Asp Leu Asn Gly Ala Ala
 145 150

<210> 10

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<222> (1)...(459)

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 1 5 10 15

gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc 96
 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
 20 25 30

agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt 144
 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
 35 40 45

gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg 192
 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
 50 55 60

gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac 240

Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn	80		
65	70	75	
acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt	288		
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val			
85	90	95	
tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc	336		
Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr			
100	105	110	
gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat	384		
Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His			
115	120	125	
cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag	432		
His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu			
130	135	140	
gat ctg aat agt gag aaa gat gag cta tgataacaat tg	471		
Asp Leu Asn Ser Glu Lys Asp Glu Leu			
145	150		
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Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln	15		
1	5	10	
Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe	30		
20	25		
Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg	45		
35	40		
Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala	60		
50	55		
Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn	80		
65	70	75	
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val	95		
85	90		
Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr	110		
100	105		
Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His	125		
115	120		

DRAFT PROTEIN SEQUENCES

His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 130 135 140

Asp Leu Asn Ser Glu Lys Asp Glu Leu
 145 150

<210> 12

<211> 38

<212> DNA

<213> Artificial

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<223> synthetic insert

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<211> 31

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<210> 15

<211> 23

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<220>

<223> synthetic insert

<400> 15

ccaattggct agcgggccat ggg

23

<210> 16

<211> 22

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 16

ccacccacga ggaaacatcg tg

22

<210> 17

<211> 39

<212> DNA

<213> Artificial

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39

<210> 18

<211> 189

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<213> Artificial

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ggattgatgt gatatctcca ctgacgtaag ggatgacgca caatcccact atccttcgca

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180

tgggaattc 189

<210> 19

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<213> Artificial

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<223> sequencing primer

<400> 19 21

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<210> 20

<211> 40

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

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<223> synthetic insert

<400> 21 35

ttcttcttgt ctctacactt ctcttattcc tagta

<210> 22

<211> 35

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 22
atatcccaact cttgccgtgc ccaggtgcag ctgca 35

<210> 23

<211> 48

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 23
gctgcacctg ggcacggcaa gagtggata ttactaggaa taagagaa 48

<210> 24

<211> 54

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

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<210> 25

<211> 24

<212> DNA

<213> Artificial

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<223> synthetic insert

<400> 25
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<210> 26

<211> 20

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 26

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20

<210> 27

<211> 107

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<223> synthetic fragment encoding PR1a leader

<220>

<221> CDS

<222> (3)..(104)

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 1 5 10 15

47

tct aca ctt ctc tta ttc cta gta ata tcc cac tct tgc cgt gcc cag
 Ser Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Gln
 20 25 30

95

gtg cag ctg cag
 Val Gln Leu

107

<210> 28

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<212> PRT

<213> Artificial

<400> 28

Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
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 20 25 30

Gln Leu

<210> 29

<211> 21

<212> DNA

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<220>

<223> PCR primer

<400> 29

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21

<210> 30

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 30

aagcttgtta acagccctta a

21

<210> 31

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 31

agggctgtta acaaacttga t

21

<210> 32

<211> 44

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 32

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<210> 33

<211> 19

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 33

aattaaccct cactaaagg 19

<210> 34

<211> 254

<212> DNA

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<220>

<221> CDS

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Thr Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn
20 25 30cat act ctg act cac aat ggt tta agg gct gtt aac aaa ctt gat ggg 143
His Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly
35 40 45ctc caa tca aga act aat act aag gta aca ccc aag atg gca tcc aga 191
Leu Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg
50 55 60act gag acc aag aga cct gga tgc tca gct acc att gtt tgt gga aaa 239
Thr Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys
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cag gtg cag ctg cag
 Gln Val Gln Leu Gln
 80

254

<210> 35

<211> 84

<212> PRT

<213> Artificial

<400> 35

Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln Thr
 1 5 10 15

Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn His
 20 25 30

Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly Leu
 35 40 45

Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg Thr
 50 55 60

Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys Gln
 65 70 75 80

Val Gln Leu Gln

<210> 36

<211> 18

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 36

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<210> 37

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<212> DNA

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<210> 38

<211> 24

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 38

cgcaagaccc ttcctctata taag

24

<210> 39

<211> 60

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 39

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60

<210> 40

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1 5 10 15Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr.
20 25

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<400> 41 atccctcaact tccaaatcaga 20

<210> 42
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<400> 42 ttcttgagag atagcttga 19

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<400> 43 gatccccatgg cccgcttagcc aattggagct 30

<210> 44
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<400> 44
`ccaattggct agcgggccat gg 22

<210> 45

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<213> Artificial

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<400> 47
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<210> 48

<211> 51

<212> DNA

<213> Artificial

<220>
 <223> PCR primer
 <400> 48
 tccAACCAAT tgTTACTATG CGGCCCCATT CAGATCCTCT TCTGAGATGA g 51

<210> 49
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> sequencing primer
 <400> 49
 gtCTGTCTAA AGTAAGTAG ATGCG 25

<210> 50
 <211> 60
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer
 <400> 50
 tccAACCAAT tgTTATCATA GCTCATCTT CTCACTATTc agATCCTCTT CTGAGATGAG 60

<210> 51
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer
 <400> 51
 agTCCCCAT ggtacgtcct gtagaaacc 29

<210> 52
 <211> 25
 <212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 52

cgtttcgtc ggtaatcacc attcc

25

<210> 53

<211> 24

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 53

cgcgaagaccc ttcctttata taag

24

<210> 54

<211> 1154

<212> DNA

<213> Artificial

<220>

<223> HCV33-hinge-CH2-CH3

<220>

<221> CDS

<222> (3)..(1136)

<400> 54

cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct
Met Glu Val Gln Leu Gln Ser Gly Gly Gly Leu Val Gln Ala
1 5 10 15

47

ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser
20 25 30

95

ggc cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys
35 40 45

143

gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp
50 55 60

191

DRAFT Sequence

tat aaa gac tcc gtg aag ggc cga tt ^c acc atc tcc aga gat aac gcc Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala 65 70 75	239
aag act acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg Lys Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr 80 85 90 95	287
gcc gtt tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc Ala Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser 100 105 110	335
ctg ccg gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val 115 120 125	383
tcc tca gaa ccc aag aca cca aaa cca caa cca caa cca caa cca caa Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln 130 135 140	431
cca caa ccc aat cct aca aca gaa tcc aag tgt ccc aaa tgt cca gcc Pro Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala 145 150 155	479
cct gag ctc ctg gga ggg ccc tca gtc ttc atc ttc ccc ccg aaa ccc Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro 160 165 170 175	527
aag gac gtc ctc tcc att tct ggg agg ccc gag gtc acg tgc gtt gtg Lys Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val 180 185 190	575
gta gac gtg ggc cag gaa gac ccc gag gtc agt ttc aac tgg tac att Val Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile 195 200 205	623
gat ggc gca gag gtg cga acg gcc aac acg agg cca aaa gag gaa cag Asp Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln 210 215 220	671
ttc aac acg acg tac cgc gtg gtc agc gtc ctg ccc atc cag cac cag Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln 225 230 235	719
gac tgg ctg acg ggg aaa gag ttc aaa tgc aag gtc aac aac aaa gct Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala 240 245 250 255	767
ctc ccg gcc ccc atc gag aag acc atc tcc aag gcc aaa ggg cag acc Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr 260 265 270	815
cg ^g gag ccg cag gtg tac gcc ctg gcc cca cac ccg gaa gag ctg gcc Arg Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala 275 280 285	863
aag gac acc gtg agc gta acc tgc ctg gtc aaa ggc ttc tac cca cct Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro 290 295 300	911
gat atc aac gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly 305 310 315	959
acc tac gcc acc acg cca ccc cag ctg gac aac gac ggg acc tac ttc Thr Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe 320 325 330 335	1007

ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag cg_g gga gaa
 Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu
 340 345 350

acc ttc acc tgt gtg gtg atg cac gag gcc ctg cac aac cac tac acc
 Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr
 355 360 365

cag aaa tcc atc acc cag tct tcg ggt aaa taa taagaattcg agctcgaa
 Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
 370 375

<210> 55

<211> 377

<212> PRT

<213> Artificial

<400> 55

Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
 1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly
 20 25 30

His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu
 35 40 45

Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr
 50 55 60

Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
 65 70 75 80

Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
 85 90 95

Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu
 100 105 110

Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125

Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro
 130 135 140

Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro
 145 150 155 160

Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 165 170 175

Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val
 180 185 190

Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp
 195 200 205

Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe
 210 215 220

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp
 225 230 235 240

Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu
 245 250 255

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg
 260 265 270

Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala Lys
 275 280 285

Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp
 290 295 300

Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr
 305 310 315 320

Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu
 325 330 335

Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr
 340 345 350

Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 355 360 365

Lys Ser Ile Thr Gln Ser Ser Gly Lys
 370 375

<210> 56

<211> 1172

<212> DNA

<213> Artificial

<220>

<223> hinge-HCV33-CH2-CH3-SEKDEL

<220>

<221> CDS

<222> (3)..(1154)

<400>	56		
cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct			47
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala			
1 5 10 15			
ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt			95
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser			
20 25 30			
ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag			143
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys			
35 40 45			
gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg			191
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp			
50 55 60			
tat aaa gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc			239
Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala			
65 70 75			
aag act acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg			287
Lys Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr			
80 85 90 95			
gcc gtt tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc			335
Ala Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser			
100 105 110			
ctg ccg gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc acc gtc			383
Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val			
115 120 125			
tcc tca gaa ccc aag aca cca aaa cca caa cca caa cca caa cca caa			431
Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln			
130 135 140			
cca caa ccc aat cct aca aca gaa tcc aag tgt ccc aaa tgt cca gcc			479
Pro Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala			
145 150 155			
cct gag ctc ctg gga ggg ccc tca gtc ttc atc ttc ccc ccg aaa ccc			527
Pro Glu Leu Leu Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro			
160 165 170 175			
aag gac gtc ctc tcc att tct ggg agg ccc gag gtc acg tgc gtt gtg			575
Lys Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val			
180 185 190			
gta gac gtg ggc cag gaa gac ccc gag gtc agt ttc aac tgg tac att			623
Val Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile			
195 200 205			
gat ggc gca gag gtg cga acg gcc aac acg agg cca aaa gag gaa cag			671
Asp Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln			
210 215 220			
ttc aac agc acg tac cgc gtg gtc agc gtc ctg ccc atc cag cac cag			719
Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln			
225 230 235			

'gac tgg ctg acg ggg aaa gag ttc aaa tgc aag gtc aac aac aaa gct 767
 Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala
 240 245 250 255
 ctc ccg gcc ccc atc gag aag acc atc tcc aag gcc aaa ggg cag acc 815
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr
 260 265 270
 cg^g gag ccg cag gtg tac gcc ctg gcc cca cac ccg gaa gag ctg gcc 863
 Arg Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala
 275 280 285
 aag gac acc gtg agc gta acc tgc ctg gtc aaa ggc ttc tac cca cct 911
 Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro
 290 295 300
 gat atc aac gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc 959
 Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly
 305 310 315
 acc tac gcc acc acg cca ccc cag ctg gac aac gac ggg acc tac ttc 1007
 Thr Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe
 320 325 330 335
 ctc tac agc aag ctc tcg gga aag aac acg tgg cag ccg gga gaa 1055
 Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu
 340 345 350
 acc ttc acc tgt gtg gtg atg cac gag gcc ctg cac aac cac tac acc 1103
 Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr
 355 360 365
 cag aaa tcc atc acc cag tct tcg ggt aaa tct gag aaa gat gag cta 1151
 Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys Ser Glu Lys Asp Glu Leu
 370 375 380
 taa taagaattcg agctcgaa 1172
 <210> 57
 <211> 383
 <212> PRT
 <213> Artificial
 <400> 57
 Met Glu Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln Ala Gly
 1 5 10 15
 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly
 20 25 30
 His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu
 35 40 45
 Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr
 50 55 60

Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
 65 70 75 80

Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
 85 90 95

Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu
 100 105 110

Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125

Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln Pro
 130 135 140

Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro
 145 150 155 160

Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 165 170 175

Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val
 180 185 190

Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp
 195 200 205

Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe
 210 215 220

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp
 225 230 235 240

Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu
 245 250 255

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg
 260 265 270

Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala Lys
 275 280 285

Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp
 290 295 300

Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr
 305 310 315 320

Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu
 325 330 335

Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr
 340 345 350

Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 355 360 365

Lys Ser Ile Thr Gln Ser Ser Gly Lys Ser Glu Lys Asp Glu Leu
 370 375 380

<210> 58

<211> 31

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 58

aggggaccca ggtcaccgc tcctcagaac c

31

<210> 59

<211> 37

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 59

gagctttgtt gttgaccttg catttgaact ctttccc

37

<210> 60

<211> 26

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 60

caa atgcaag gtcaacaaca aagctc

26

<210> 61

<211> 42
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<400> 61
ttcgagctcg aattcttatt atttacccga agactgggtg at 42

<210> 62
<211> 27
<212> DNA
<213> Artificial

<220>
<223> sequencing primer
<400> 62
ctgaggagac ggtgacctgg gtccccct 27

<210> 63
<211> 46
<212> DNA
<213> Artificial

<220>
<223> PCR primer
<400> 63
agccccctgag ctcctggag ggccctcagt ctcatcttc cccccc 46

<210> 64
<211> 61
<212> DNA
<213> Artificial

<220>
<223> PCR primer
<400> 64
ttcgagctcg aattcttatt atttacccga agactgggtg atggatttct gggtgttagtg 60

<210> 65

<211> 79

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 65

ttcgagctcg aattcttatt atagctcatc tttctcagat ttacccgaag actgggtgat 60

ggatttctgg gtgttagtgg

79

<210> 66

<211> 461

<212> DNA

<213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (3) .. (449)

<400> 66

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1 5 10 15gct ggg ggg tct ctg agg ctc tcc tgt gca gcc tct gga agc att ttc 95
Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe
20 25 30aga cgt ccg cat atg ggt tgg ttc cgc cag gct cca ggg cag gag cgc 143
Arg Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg
35 40 45gag ttg gtc gca ctg att tct gcg ggt cgt aca tgg tat gca gac 191
Glu Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp
50 55 60tcc gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg 239
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
65 70 75

ctg tat ctg caa atg aac aac agc ctg aaa cct gag gac acg gcc gtt tat 287

Leu Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr
 80 85 90 95

tac tgt act gcc ggg ggt tcg tac tgg ggc cag ggg acc cag cag gtc acc
 Tyr Cys Thr Ala Gly Gly Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110

gtc gcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc gcc cat
 Val Ala Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala Ala His
 115 120 125

cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag
 His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 130 135 140

gat ctg aat ggg gcc gca tagtaacaat tg 431
 Asp Leu Asn Gly Ala Ala
 145

<210> 67

<211> 149

<212> PRT

<213> Artificial

<400> 67

Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
 1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Arg
 20 25 30

Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg Glu
 35 40 45

Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp Ser
 50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu
 65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Thr Ala Gly Gly Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
 100 105 110

Ala Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala Ala His His
 115 120 125

His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp
 130 135 140

Leu Asn Gly Ala Ala
145

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